WE CLAIM:

1. An isolated polynucleotide from coryneform bacteria containing a polynucleotide sequence coding for the sigC gene, selected from the group

   a) a polynucleotide that is at least 70% identical to a polynucleotide coding for a polypeptide that contains the amino acid sequence of SEQ ID No. 2,

   b) a polynucleotide coding for a polypeptide that contains an amino acid sequence that is at least 70% identical to the amino acid sequence of SEQ ID No. 2,

   c) a polynucleotide that is complementary to the polynucleotides of a) or b), and

   d) a polynucleotide containing at least 15 successive nucleotides of the polynucleotide sequence of a), b) or c).

2. The polynucleotide according to claim 1, wherein the polypeptide has sigma factor C activity.

3. The polynucleotide according to claim 1, wherein the polynucleotide is a recombinant DNA replicable in coryneform bacteria.

4. The polynucleotide according to claim 1, wherein the polynucleotide is an RNA.

5. The polynucleotide according to claim 3, containing the nucleic acid sequence as shown in SEQ ID No. 1.

6. The polynucleotide according to claim 3, wherein the DNA, comprises

   (i) the nucleotide sequence shown in SEQ ID No. 1, or

(ii) at least one sequence that corresponds to the sequence (i) within the region of degeneracy of the genetic code, or

(iii) at least one sequence that hybridizes with the sequence that is complementary to the sequence (i) or (ii), and optionally

7. The polynucleotide according to claim 6, further comprising

(iv) functionally neutral sense mutations in (i).

8. The polynucleotide according to claim 6, wherein the hybridization of sequence (iii) is carried out under conditions of stringency corresponding at most to 2x SSC.

9. The polynucleotide sequence according to claim 3, that codes for a polypeptide that contains the amino acid sequence shown in SEQ ID No. 2.

10. A coryneform bacteria, in which the sigC gene is enhanced.

11. The coryneform bacteria according to claim 10, wherein the sigC gene is overexpressed.

12. An Escherichia coli strain DH5αmcr/pEC-XK99EsigCb2ex filed as DSM 14375.

13. A Corynebacterium glutamicum strain DSM5715/pEC-XK99E filed as DSM 13455.

14. A method for the enzymatic production of L-amino acids in coryneform bacteria comprising:

a) fermenting, in a medium, the coryneform bacteria which produce the desired L-amino acid and in which at least the sigC gene or nucleotide sequences coding for the latter are enhanced.

15. The method according to claim 14, further comprising:

b) enriching the L-amino acid in the medium or in the cells of the bacteria.

16. The method according to claim 15, further comprising:

c) isolating the L-amino acid.

17. The method according to claim 14, wherein the L amino acids are lysine.

18. The method according to claim 14, wherein coryneform bacteria in which at least the sigC gene or nucleotide sequences coding for the latter are overexpressed are fermented.

19. The method according to claim 14, wherein additional genes of the biosynthesis pathway of the desired L-amino acid are enhanced in the bacteria.

20. The method according to claim 14, wherein additional genes of the biosynthesis pathway of the desired L-amino acid are enhanced in the bacteria

21. The method according to claim 14, wherein a strain transformed with a plasmid vector is used, and the plasmid vector carries the nucleotide sequence coding for the sigC gene.

22. The method according to claim 14, wherein the polynucleotide(s) that code(s) for the sigC gene is enhanced.

23. The method according to claim 22, wherein the polynucleotide(s) that code(s) for the sigC gene is overexpressed.

24. The method according to claim 14, wherein the regulatory properties of the polypeptide for which the polynucleotide sigC codes are raised.

25. The method according to claim 14, wherein the bacteria being fermented comprise, at the same time, one or more genes which are enhanced; wherein the one or more genes is/are selected from the group consisting of:

the gene dapA coding for dihydrodipicolinate synthase,

the gene gap coding for glyceraldehyde-3-phosphate dehydrogenase,

the gene tpi coding for triosephosphate isomerase,

the gene pgk coding for 3-phosphoglycerate kinase,

the gene zwf coding for glucose-6-phosphate dehydrogenase,

the gene pyc coding for pyruvate carboxylase,

the gene mqo coding for malate-quinone-oxidoreductase,

the gene lysC coding for a feedback-resistant aspartate kinase,

the gene lysE coding for lysine export,

the gene hom coding for homoserine dehydrogenase,

the gene ilvA coding for threonine dehydratase or the allele ilvA(Fbr) coding for a feedback-resistant threonine dehydratase,

the gene ilvBN coding for acetohydroxy acid synthase,

the gene ilvD coding for dihydroxy acid dehydratase,and

the gene zwal coding for the Zwa1 protein.

26. Process according to claim 14, wherein the bacteria being fermented comprise, at the same time, one or more genes which are attenuated; wherein the genes are selected from the group consisting of:

the gene pck coding for phosphoenol pyruvate carboxykinase,

the gene pgi coding for glucose-6-phosphate isomerase,

the gene poxB coding for pyruvate oxidase, and

the gene zwa2 coding for the Zwa2 protein.

27. The method according to claim 14 wherein microorganisms of the genus Corynebacterium are used.

28. The method according to claim 27, wherein the Corynebacterium glutamicum strain DH5αmcr/pEC-XK99EsigCb2ex is used.

29. The method according to claim 27, wherein the Corynebacterium glutamicum strain DSM5715/pEC-XK99E is used.

30. Coryneform bacteria containing a vector that carries a polynucleotide according to claim 1.

31. A method for discovering RNA, cDNA and DNA in order to isolate nucleic acids or polynucleotides or genes that code for the sigma factor C or that have a high degree of similarity to the sequence of the sigC gene, comprising contacting the RNA, cDNA, or DNA with hybridization probes comprising polynucleotide sequences according to claim 1.

32. The method according to claim 31, wherein arrays, micro arrays or DNA chips are used.